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Sequence Listing was accepted.

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Reviewer: Durreshwar Anjum

Timestamp: [year=2010; month=3; day=30; hr=14; min=53; sec=12; ms=838; ]

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Application No: 10587723

Version No: 1.0

Input Set:

Output Set:

Started: 2010-03-23 14:30:29.458

Finished: 2010-03-23 14:30:33.533

Elapsed: 0 hr(s) 0 min(s) 4 sec(s) 75 ms

Total Warnings: 212

Total Errors: 0

No. of SeqIDs Defined: 212

Actual SeqID Count: 212

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**Input Set:**

**Output Set:**

**Started:** 2010-03-23 14:30:29.458  
**Finished:** 2010-03-23 14:30:33.533  
**Elapsed:** 0 hr(s) 0 min(s) 4 sec(s) 75 ms  
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Error code

Error Description

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<110> MILLER, JEFFREY C.  
 ZHANG, LEI

<120> METHODS AND COMPOSITIONS FOR TARGETED CLEAVAGE AND RECOMBINATION

<130> 8325-0036.31

<140> 10587723  
 <141> 2010-03-23

<150> PCT/US04/25407  
 <151> 2004-08-06

<150> 60/542,780  
 <151> 2004-02-05

<150> 60/556,831  
 <151> 2004-03-26

<150> 60/575,919  
 <151> 2004-06-01

<150> 10/912,932  
 <151> 2004-08-06

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ccctgtggag ccacacccta gggttggcca atctactccc aggagcaggg agggcaggag	180
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 acttagacct caccctgtgg agccacaccc tagggttggc caatctactc ccaggagcag 240  
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Ser Arg Ser Asp Asn Leu Ser Glu His Ile Arg Thr His Thr Gly Glu  
35 40 45

Lys Pro Phe Ala Cys Asp Ile Cys Gly Arg Lys Phe Ala Arg Asn Ala  
50 55 60

His Arg Ile Asn His Thr Lys Ile His Thr Gly Ser Gln Lys Pro Phe  
65 70 75 80

Gln Cys Arg Ile Cys Met Arg Asn Phe Ser Arg Ser Asp Thr Leu Ser  
85 90 95

Glu His Ile Arg Thr His Thr Gly Glu Lys Pro Phe Ala Cys Asp Ile  
100 105 110

Cys Gly Arg Lys Phe Ala Ala Arg Ser Thr Arg Thr Thr His Thr Lys  
115 120 125

Ile His Leu Arg Gln Lys Asp Ala Ala Arg Gly Ser Gln Leu Val Lys  
130 135 140

Ser Glu Leu Glu Glu Lys Lys Ser Glu Leu Arg His Lys Leu Lys Tyr  
145 150 155 160

Val Pro His Glu Tyr Ile Glu Leu Ile Glu Ile Ala Arg Asn Ser Thr  
165 170 175

Gln Asp Arg Ile Leu Glu Met Lys Val Met Glu Phe Phe Met Lys Val  
180 185 190

Tyr Gly Tyr Arg Gly Lys His Leu Gly Gly Ser Arg Lys Pro Asp Gly  
195 200 205

Ala Ile Tyr Thr Val Gly Ser Pro Ile Asp Tyr Gly Val Ile Val Asp  
210 215 220

Thr Lys Ala Tyr Ser Gly Gly Tyr Asn Leu Pro Ile Gly Gln Ala Asp  
225 230 235 240

Glu Met Gln Arg Tyr Val Glu Glu Asn Gln Thr Arg Asn Lys His Ile  
245 250 255

Asn Pro Asn Glu Trp Trp Lys Val Tyr Pro Ser Ser Val Thr Glu Phe  
260 265 270

Lys Phe Leu Phe Val Ser Gly His Phe Lys Gly Asn Tyr Lys Ala Gln  
275 280 285

Leu Thr Arg Leu Asn His Ile Thr Asn Cys Asn Gly Ala Val Leu Ser  
290 295 300

Val Glu Glu Leu Leu Ile Gly Gly Glu Met Ile Lys Ala Gly Thr Leu  
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20 25 30

Ser Arg Ser Asp Ser Leu Ser Arg His Ile Arg Thr His Thr Gly Glu  
35 40 45

Lys Pro Phe Ala Cys Asp Ile Cys Gly Arg Lys Phe Ala Asp Ser Ser  
50 55 60

Asn Arg Lys Thr His Thr Lys Ile His Thr Gly Gly Gly Gly Ser Gln  
65 70 75 80

Lys Pro Phe Gln Cys Arg Ile Cys Met Arg Asn Phe Ser Arg Ser Asp  
85 90 95

Ser Leu Ser Val His Ile Arg Thr His Thr Gly Glu Lys Pro Phe Ala  
100 105 110

Cys Asp Ile Cys Gly Arg Lys Phe Ala Asp Arg Ser Asn Arg Ile Thr  
115 120 125

His Thr Lys Ile His Leu Arg Gln Lys Asp Ala Ala Arg Gly Ser Gln  
130 135 140

Leu Val Lys Ser Glu Leu Glu Glu Lys Lys Ser Glu Leu Arg His Lys  
145 150 155 160

Leu Lys Tyr Val Pro His Glu Tyr Ile Glu Leu Ile Glu Ile Ala Arg  
165 170 175

Asn Ser Thr Gln Asp Arg Ile Leu Glu Met Lys Val Met Glu Phe Phe  
180 185 190

Met Lys Val Tyr Gly Tyr Arg Gly Lys His Leu Gly Gly Ser Arg Lys  
195 200 205

Pro Asp Gly Ala Ile Tyr Thr Val Gly Ser Pro Ile Asp Tyr Gly Val  
210 215 220

Ile Val Asp Thr Lys Ala Tyr Ser Gly Gly Tyr Asn Leu Pro Ile Gly  
225 230 235 240

Gln Ala Asp Glu Met Gln Arg Tyr Val Glu Glu Asn Gln Thr Arg Asn  
245 250 255

Lys His Ile Asn Pro Asn Glu Trp Trp Lys Val Tyr Pro Ser Ser Val  
260 265 270

Thr Glu Phe Lys Phe Leu Phe Val Ser Gly His Phe Lys Gly Asn Tyr  
275 280 285

Lys Ala Gln Leu Thr Arg Leu Asn His Ile Thr Asn Cys Asn Gly Ala  
290 295 300

Val Leu Ser Val Glu Glu Leu Leu Ile Gly Gly Glu Met Ile Lys Ala  
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Gly Thr Leu Thr Leu Glu Glu Val Arg Arg Lys Phe Asn Asn Gly Glu  
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ctgacctacg gcgtgcagtg cttcagccgc taccctgacc acatgaagca gcacgacttc 240

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aacttcaaga tccgccacia catcgaggac ggtagcgtgc agctcgccga cactaccag 540

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